

Fusing Omics and Advanced Cell Models: A New Era for Drug Discovery and Reproducibility

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About ATCC®



- Founded in 1925, ATCC® is a non-profit organization with HQ in Manassas, VA, and an R&D and Services center in Gaithersburg, MD
- World's premier biological materials resource and standards development organization
- 5,000+ cell lines
- 80,000 microorganisms
- Genomic & synthetic nucleic acids
- Media/reagents
- ATCC® collaborates with and supports the scientific community with industry-standard biological products and innovative solutions
- Growing portfolio of products and services
- Sales and distribution in 150 countries, 20 international distributors
- Talented team of 600+ employees, over one-third with advanced degrees



Agenda



1

Why reference-quality OMICS data matters

2

Introducing ATCC® Cell Line Land: Building a trusted OMICS repository

3

Empowering discovery with ATCC® Cell Line Land



Common challenges in biopharma R&D



"Finding the right cell lines for my research is a challenge."



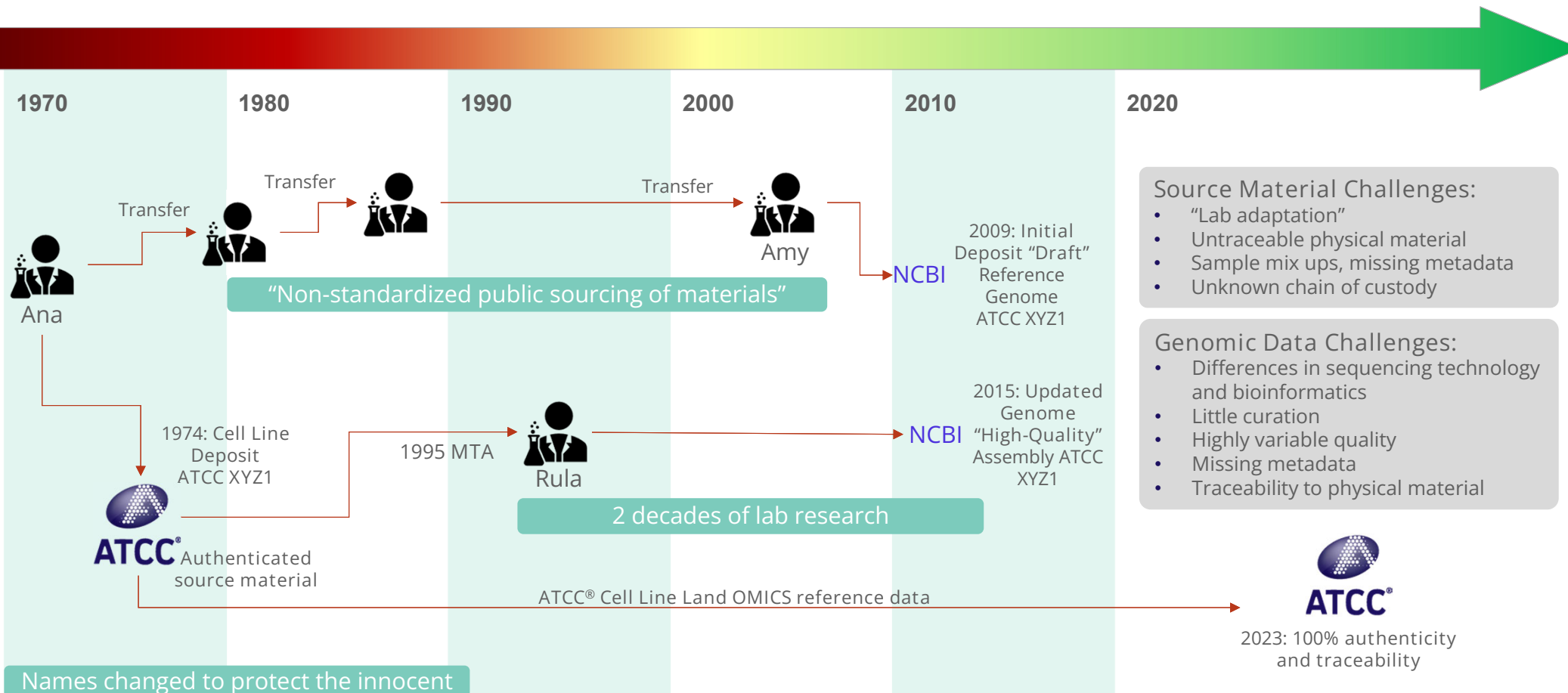
"Many cell types are not good models for the disease I'm studying."



"Pre-existing results are difficult to reproduce and often not reproducible."

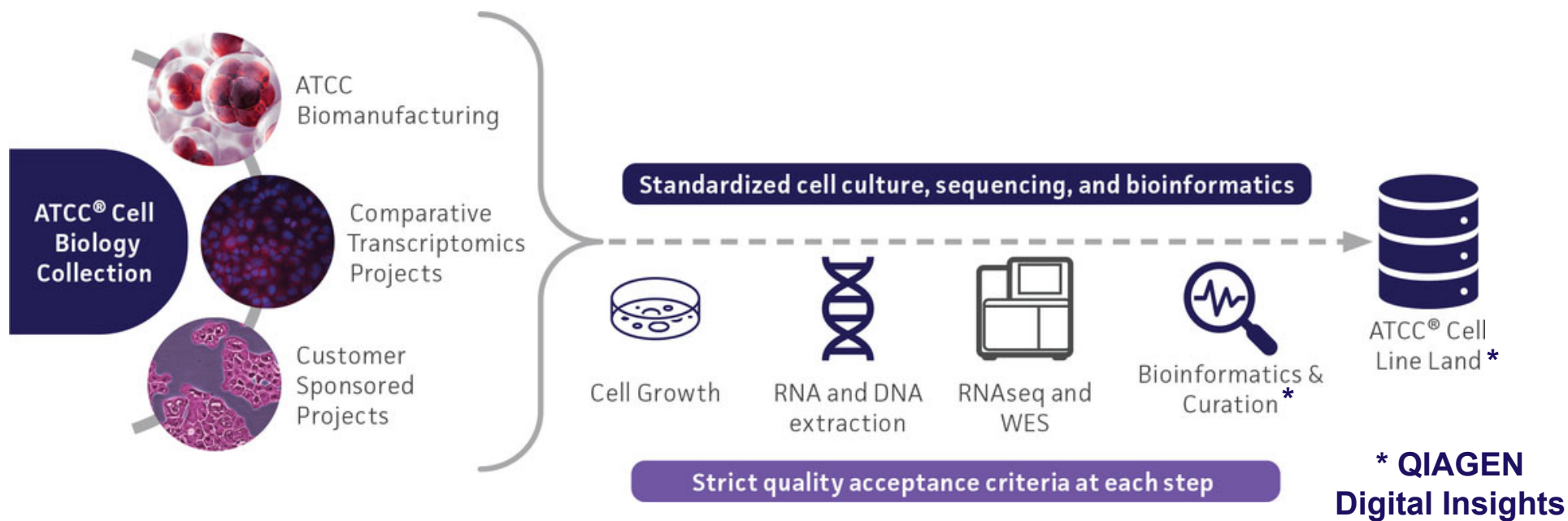
In a 2015 publication by Freedman et al., an analysis of past studies indicated that 50% of preclinical research was not reproducible. One of the main factors driving non-reproducible research is the use of unauthenticated biological reagents and reference materials.

Challenges when using public genomic data



ATCC Cell Line Land

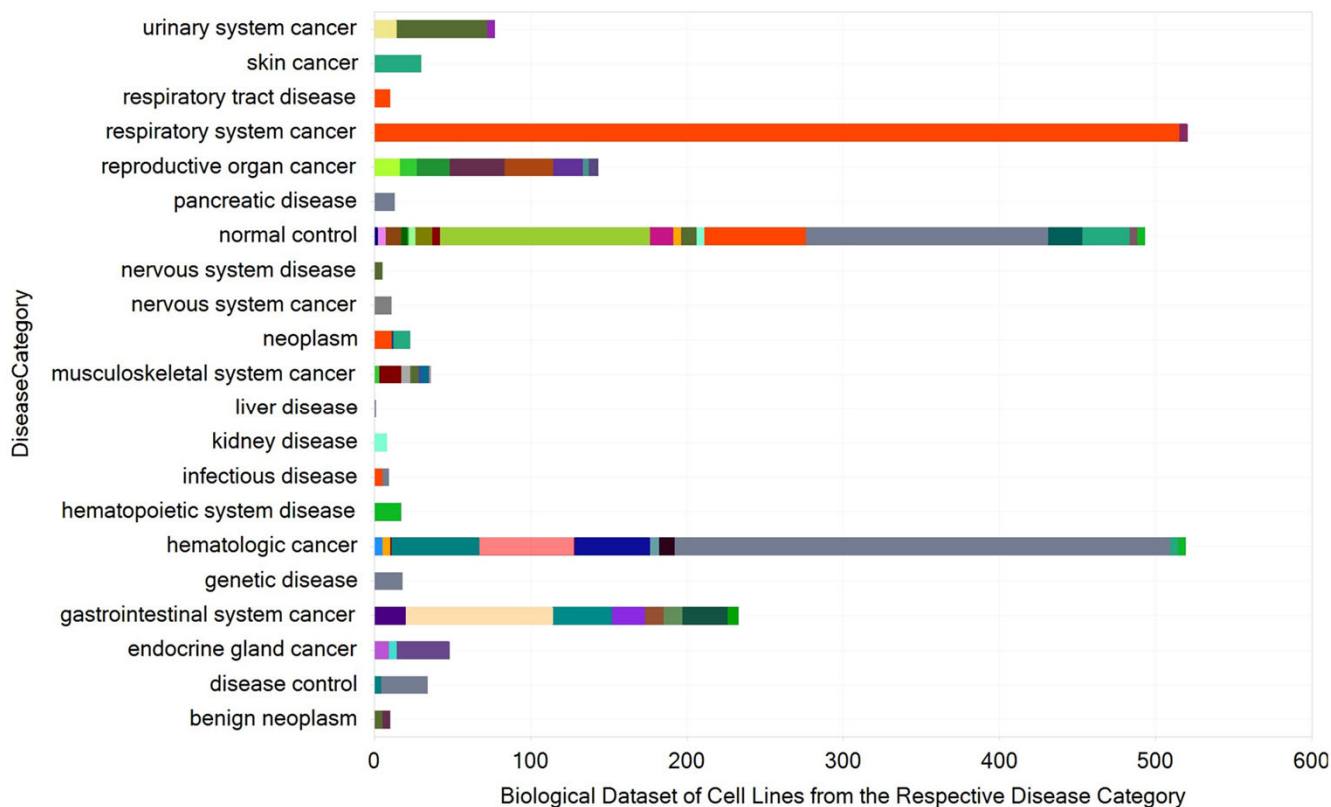
Addressing common challenges in biopharma R&D



Ensuring the highest standards of data quality, reproducibility, and traceability to the existing physical materials.

ATCC cell lines RNA-seq data atlas

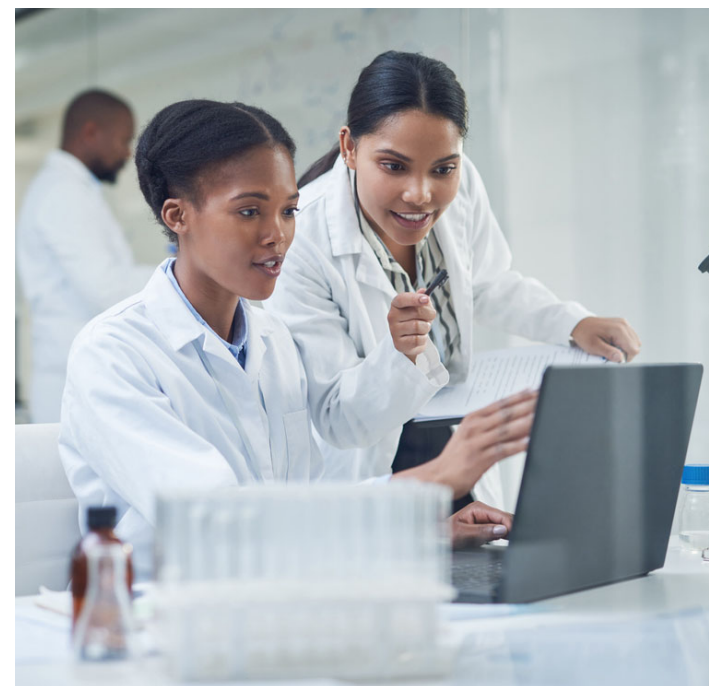
Over 600 human cell across various tissue and disease types completed



Innovating with ATCC Cell Line Land omics data

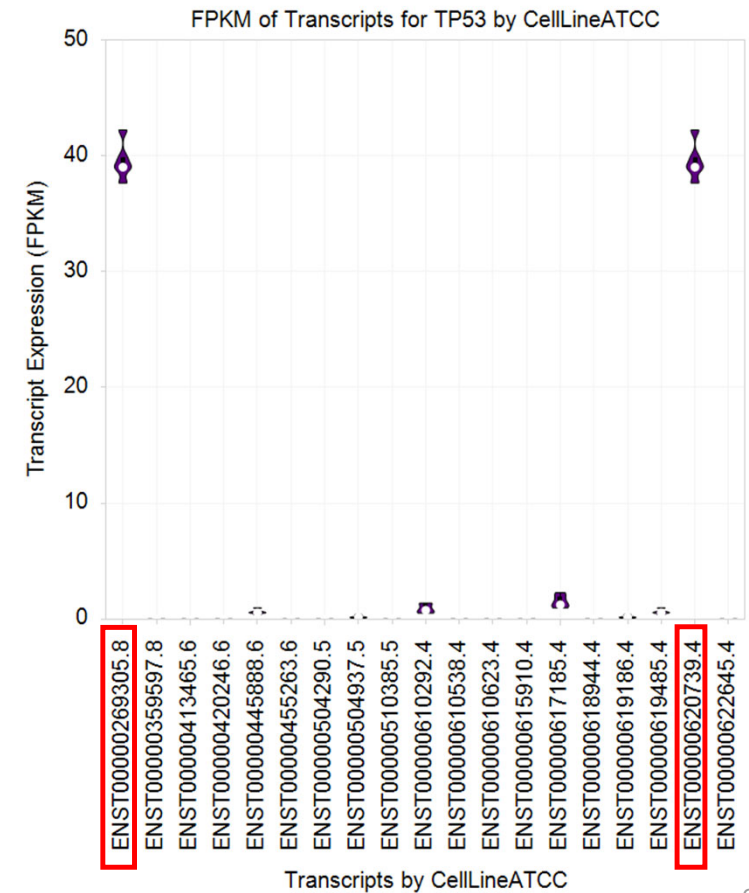
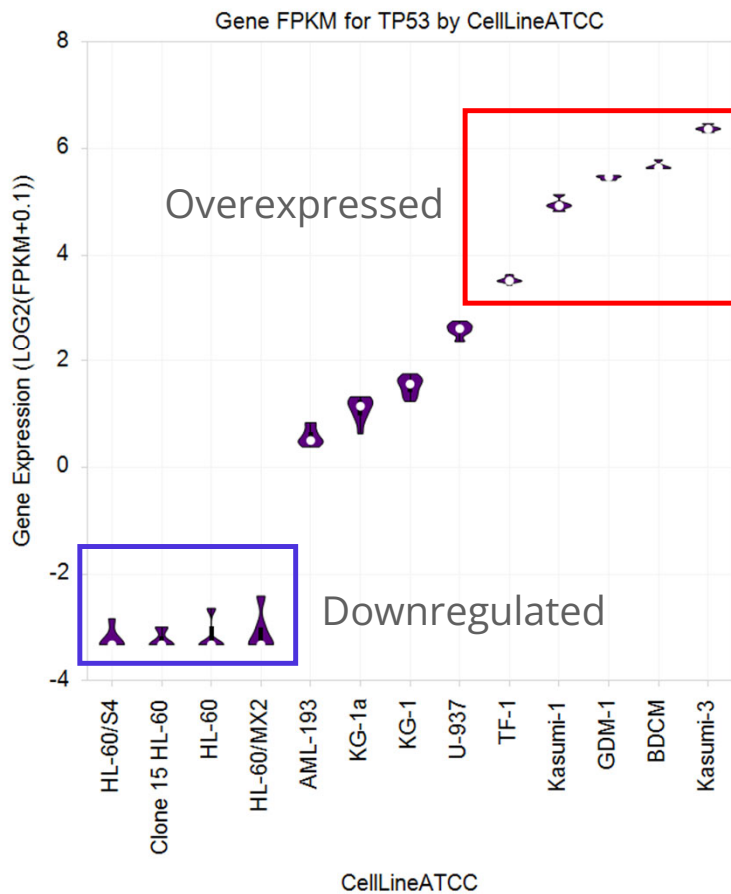


-  Compare gene expression across or within cell lines
-  Explore precomputed differential gene expression
-  Analyze pathway and gene interactomes
-  Discover biomarkers and therapeutic targets
-  Predict drug treatment responses
-  Investigate molecular mechanisms of disease pathogenesis
-  Use as a reference control in your experimental setting
-  Build hypothesis and design experiments
-  Make data-driven selections of suitable cell lines



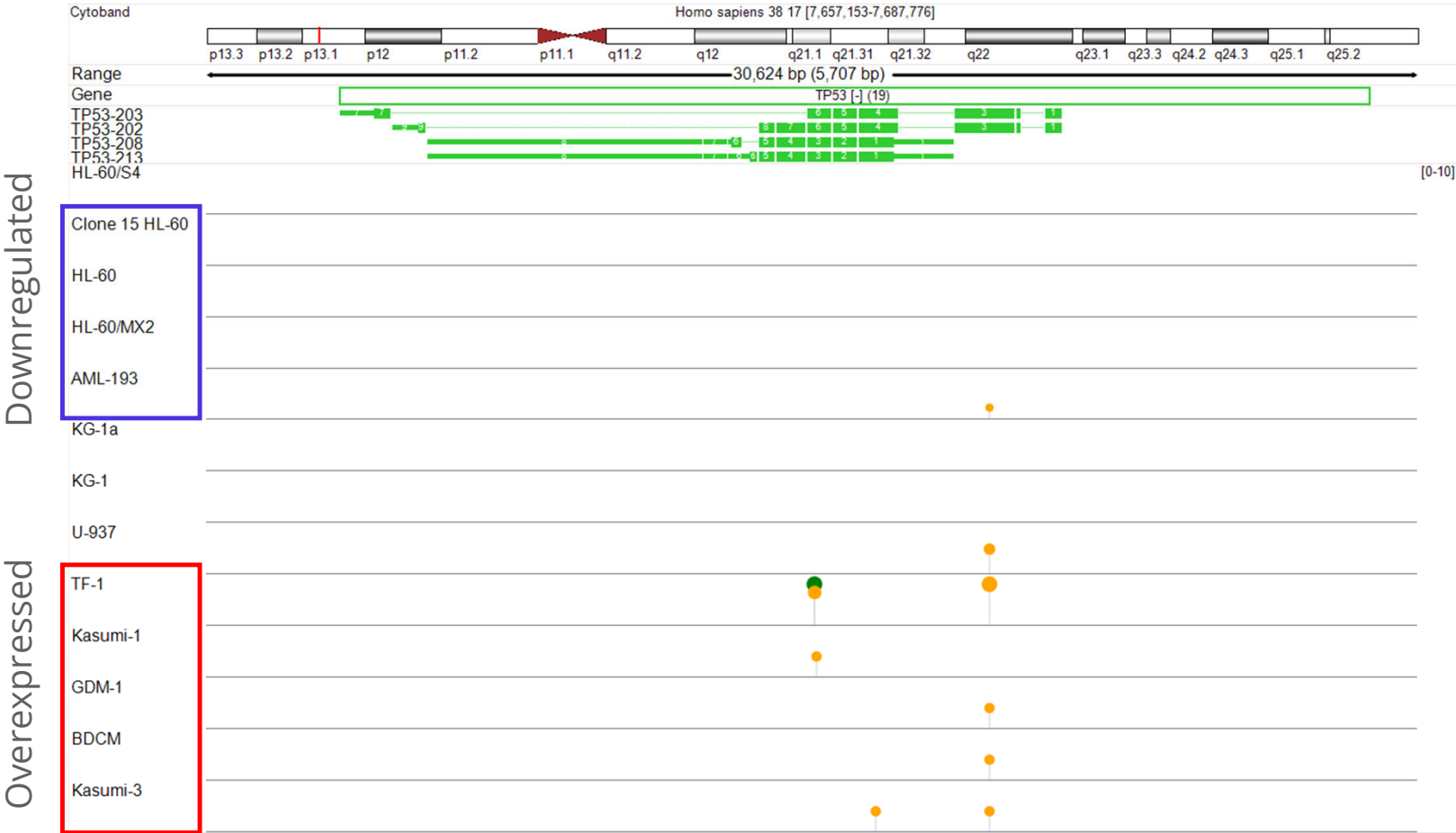
Select cell lines for target gene expression

P53 expression profile in acute myeloid leukemia cell lines



Identify cell lines with specific coding mutations

Mutations in TP53 gene are common in various hematological malignancies



Colors

- Deletion
- Non-Synonymous

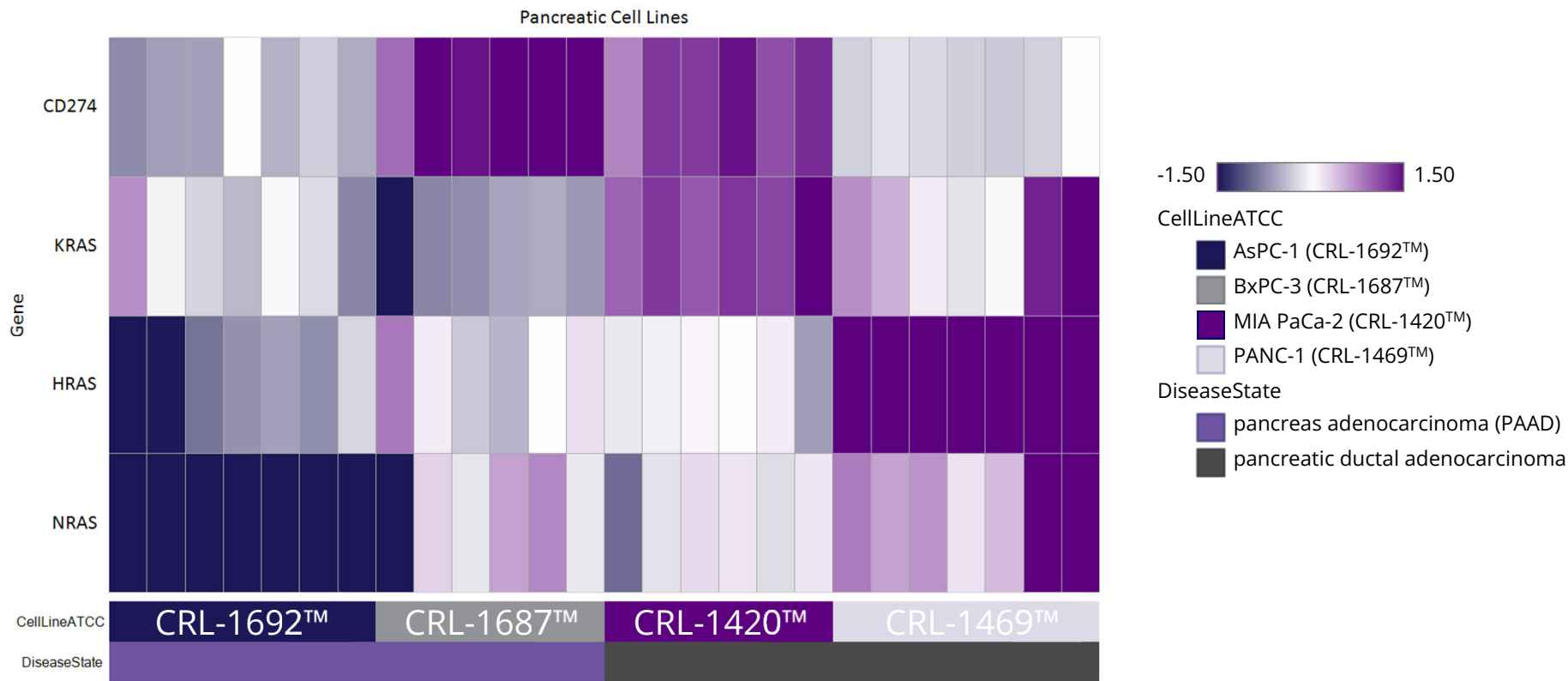
Slide 10

HK0

Match color of box around cell line name to match slide 9 - the ones with lower tp53 expression also lack the exon 3 mutation

Hrisavgi Kondilis Mangum - QIAG, 2025-06-11T17:22:31.282

Predict drug sensitivity response of cell lines



Slide 11

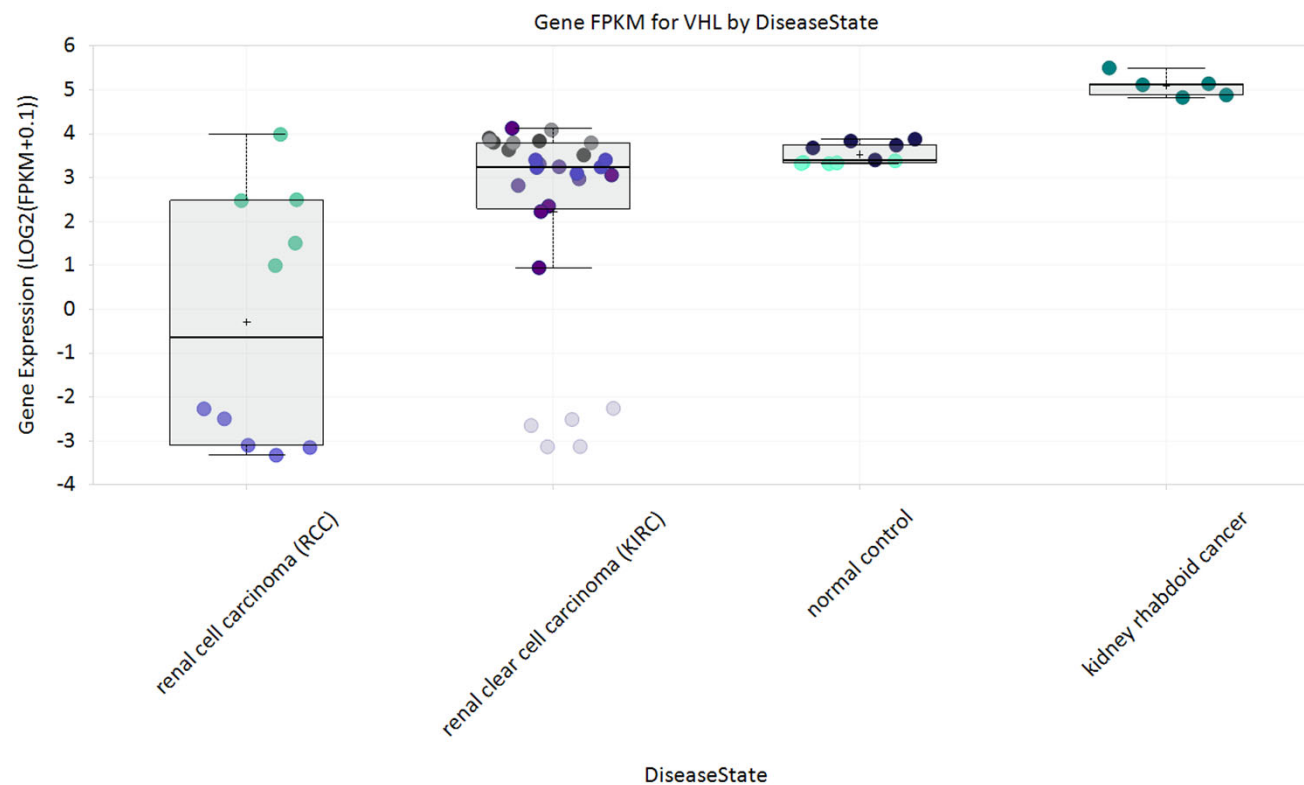
HK0

Increased font size. Is this big enough?

Hrisavgi Kondilis Mangum - QIAG, 2025-06-11T17:11:37.109

Evaluate differential gene expression analysis

Normal versus cancerous tissues



Color by CellLineATCC

- 769-P (CRL-1933™)
- 786-O [786-O] (CRL-1932™)
- A-498 (HTB-44™)
- A-704 (HTB-45™)
- ACHN (CRL-1611™)
- Caki-1 (HTB-46™)
- Caki-2 (HTB-47™)
- CCD 1103 KIDTr (CRL-2305™)
- G-401 (CRL-1441™)
- Hs 835.T (CRL-7569™)
- Primary Renal Cortical Epithelial Cells (HRCE) (PCS-400-011™, Normal Control)

Slide 12

MM0 The fonts on this table and the legend are really small. Can you increase the font size?

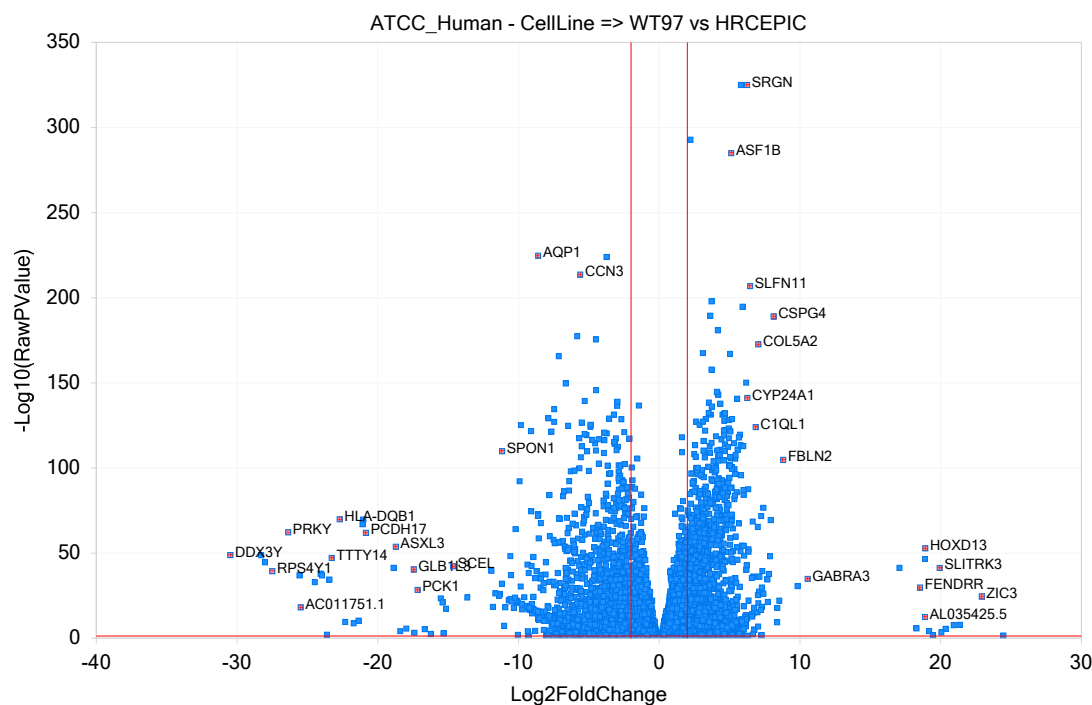
Muskus, Michael, 2025-04-16T13:20:11.155

HK0 0 Increased font for legend. Do we need to increase rest of figure?

Hrisavgi Kondilis Mangum - QIAG, 2025-06-11T17:12:02.982

Identify key differentially expressed genes

Polycystic kidney disease (PKD)



HQ0

Chronic kidney disease (CKD) affects more than 840 million people worldwide

Polycystic Kidney Disease ADPKD, WT- 9-7 (ATCC® CRL-2830™)

Primary Renal Cortical Epithelial Cells; Normal, Human (HRCE) (ATCC® PCS-400-011™)

Slide 13

HQ0 important to state the number of samples per group
Hrisavgi Kondilis Mangum - QIAG, 2025-06-11T16:41:45.664

Use case: From real world data to cell line selection

How ATCC Cell Line Land enables scientist to make data driven decisions

Gene signature for an aggressive subset of tumors that respond well to immunotherapies

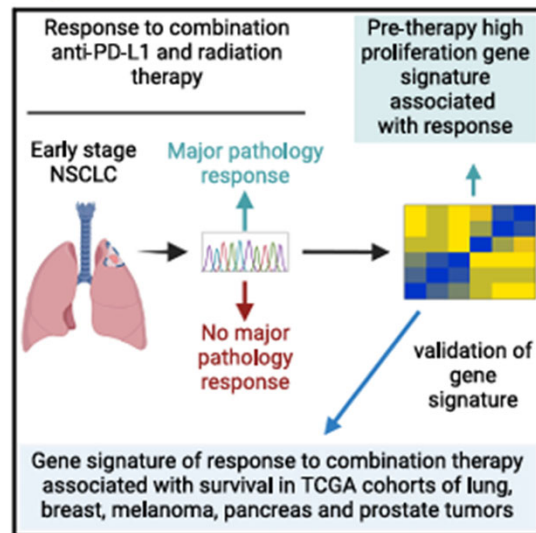


Cell Reports
Medicine

Article

A signature of enhanced proliferation associated with response and survival to anti-PD-L1 therapy in early-stage non-small cell lung cancer

Graphical abstract



Authors

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Correspondence

nkaltork@med.cornell.edu (N.K.A.), temcgraw@med.cornell.edu (T.E.M.)

In brief

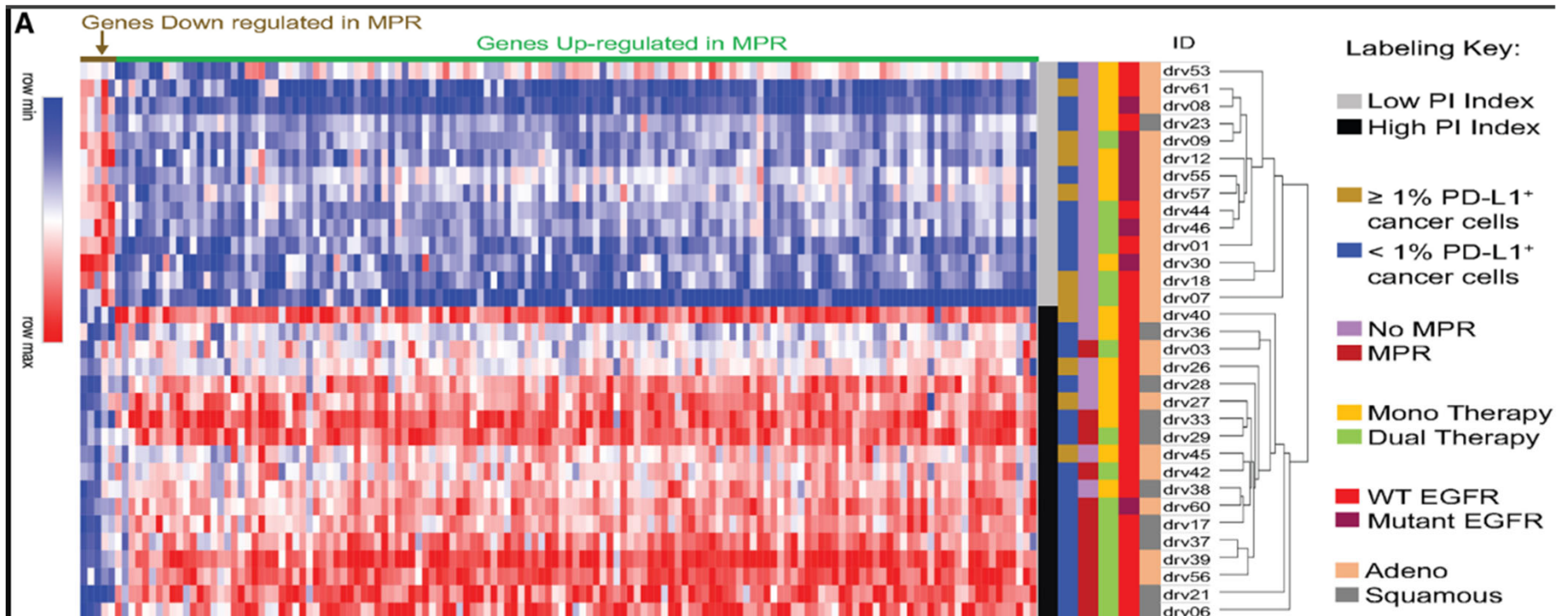
Altorki et al. identify a 140-gene signature, reflecting a high proliferation index of tumor cells, that identifies a molecular subclass of early-stage lung tumors that are more responsive to anti-PD-L1 subablative SBRT therapy. A similar molecular subclass of other solid tumors may be more likely to respond to immunotherapies.

Highlights

- High proliferation index (PI) tumors have an immunosuppressive microenvironment
- High PI NSCLC responds to combination anti-PDL1 and low-dose radiation therapy
- High PI tumors have improved survival to ICB alone and to the combination therapy
- High PI subclasses of TCGA solid tumors are associated with survival

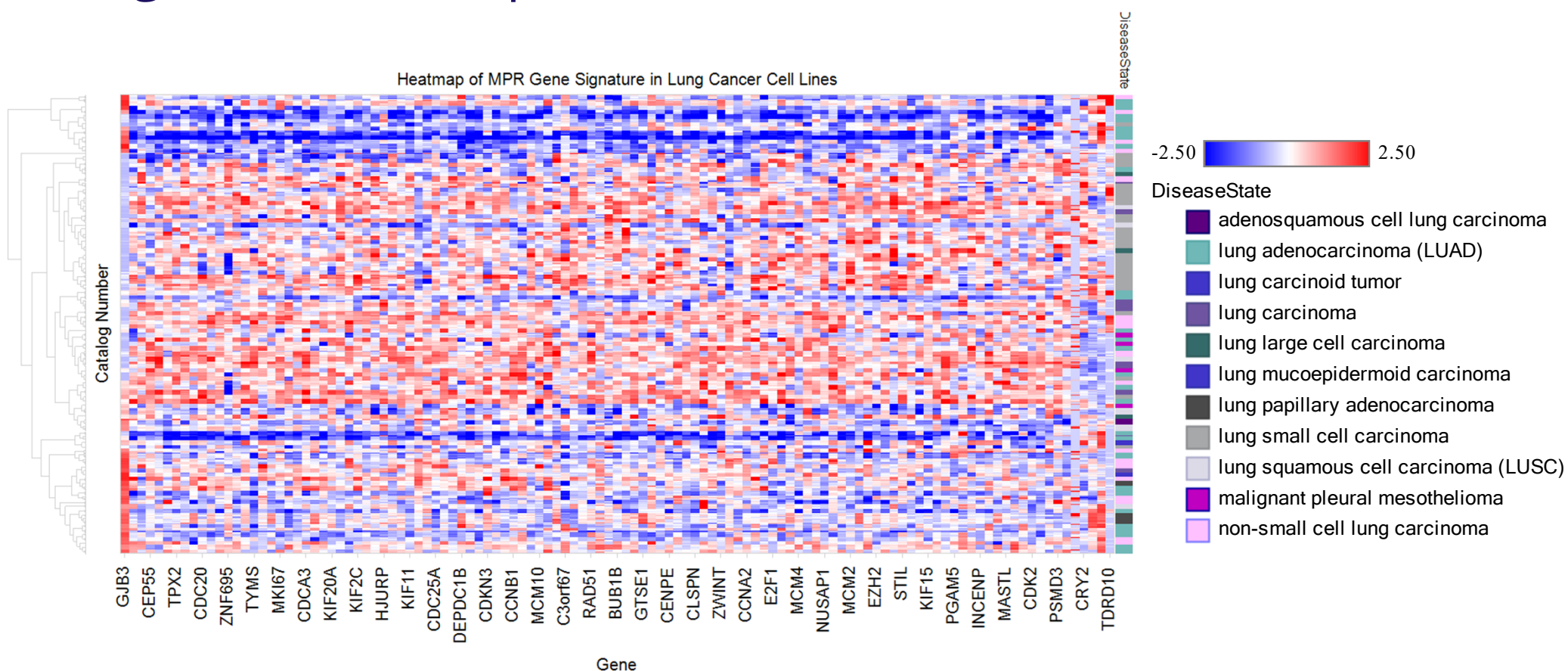
[https://www.cell.com/cell-reports-medicine/fulltext/S2666-3791\(24\)00061-2](https://www.cell.com/cell-reports-medicine/fulltext/S2666-3791(24)00061-2)

Genes are upregulated in samples with major pathologic response (MPR)

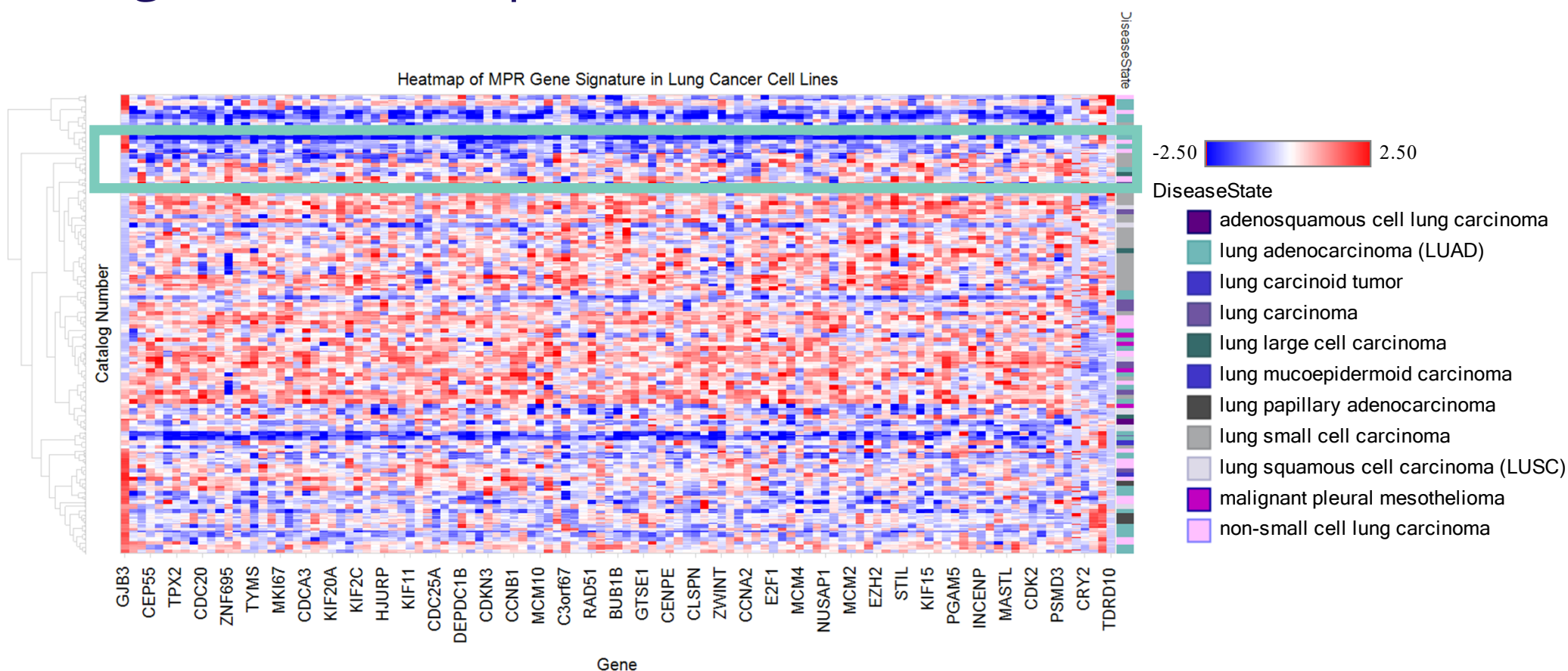


[https://www.cell.com/cell-reports-medicine/fulltext/S2666-3791\(24\)00061-2](https://www.cell.com/cell-reports-medicine/fulltext/S2666-3791(24)00061-2)

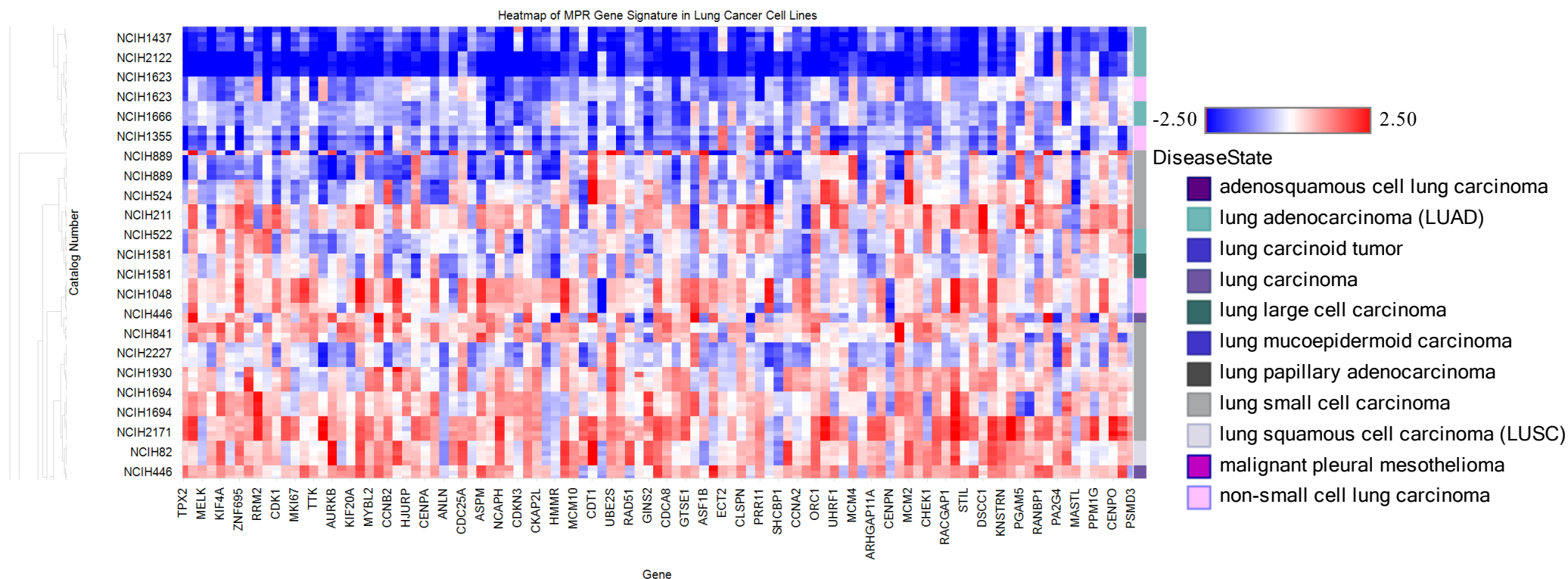
Choose cell lines to study this gene signature of response



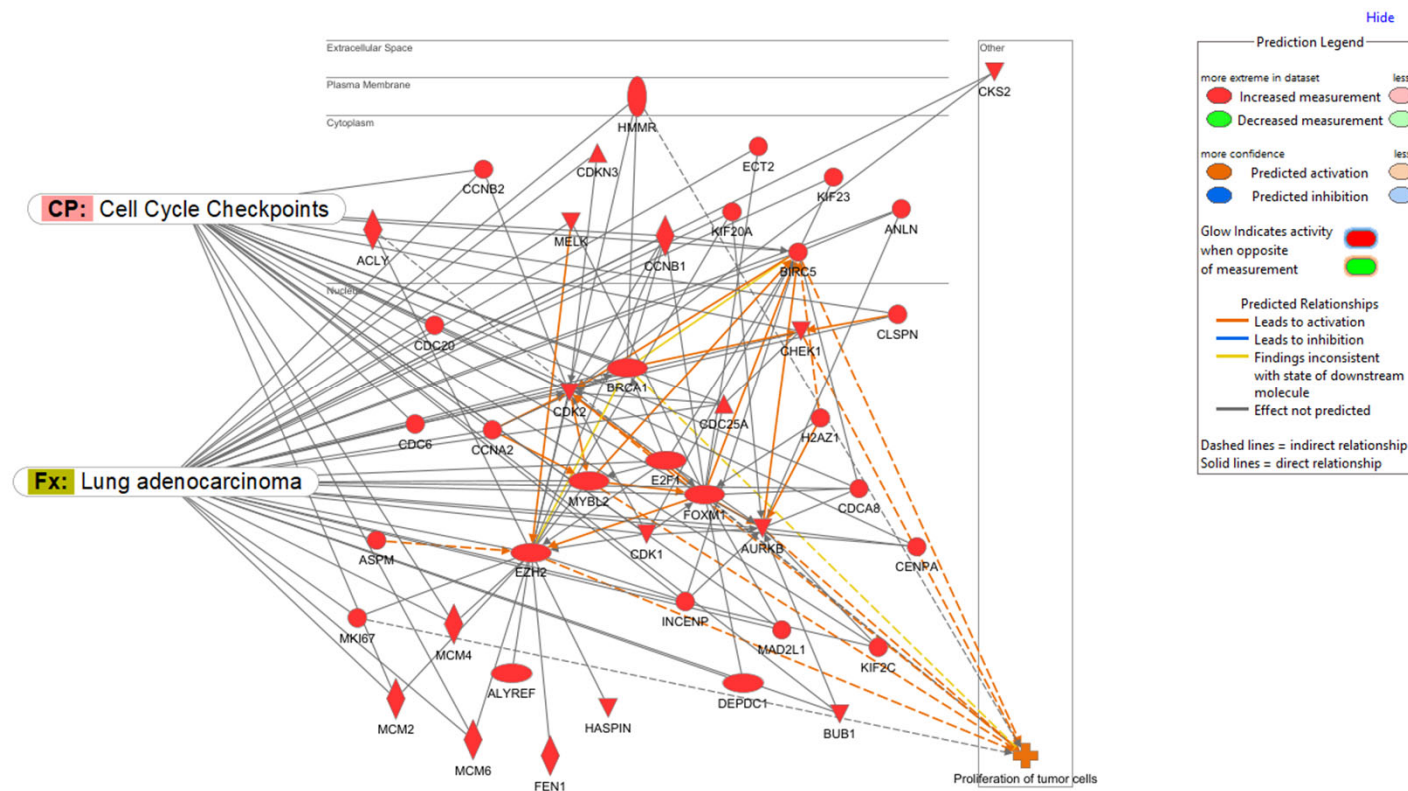
Choose cell lines to study this gene signature of response



Choose cell lines to study this gene signature of response



IPA shows enrichment for cell cycle checkpoints pathways and various lung cancer indications



Summary



- ATCC® Cell Line Land is a trusted OMICS data resource built on authenticated ATCC cell lines, offering traceable and high-quality reference datasets.
- By integrating genomic data with authenticated biological materials, the platform drives innovation and supports faster, more reliable drug discovery and development.
- All data is generated using a standardized, ISO 9001-compliant workflow to ensure scientific rigor and reproducibility.
- The platform is continuously expanding, with over 200 new cell line datasets added each year through quarterly updates.



Visit ATCC Cell
Line Land



Learn more about our
transcriptomics data

Quick Links

- ATCC Transcriptomic General Information: www.atcc.org/transcriptomics
- ATCC Cell Line Land Website: <https://digitalinsights.qiagen.com/atcc-cell-line-land/>
- OmicSoft Website: <https://digitalinsights.qiagen.com/products-overview/discovery-insights-portfolio/qiagen-omicsoft/>
 - Software used for data processing, analysis and visualization
- IPA Website: <https://digitalinsights.qiagen.com/products-overview/discovery-insights-portfolio/analysis-and-visualization/qiagen-ipa/>
 - Software used for biological interpretation and pathway analysis



CREDIBLE LEADS TO INCREDIBLE

Thank You

ATCC® Cell Line Land (ACLL) – Your go-to resource for answering the most critical questions in pre-clinical research with confidence, clarity, and credibility.